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PCT/DE99/02865

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SEQUENCE LISTING

GENERAL INFORMATION:

APPLICANT:

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COUNTRY: Germany  
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REPRESENTATIVE:

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COUNTRY: Germany  
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REGISTRATION NUMBER: 246 263  
FILE NUMBER: km-1/pct

TELECOMMUNICATIONS:

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TITLE OF THE INVENTION

Regulatory Protein from Human Keratinocytes

NUMBER OF SEQUENCES 4

COMPUTER-READABLE VERSION

DATA CARRIER: diskette  
COMPUTER: IBM-compatible PC  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word for Windows 6.0

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DETAILS FOR SEQ ID NO 1

SEQUENCE CHARACTERISTICS

LENGTH:	2533 Base Pairs
TYPE:	deoxyribonucleic acid
TOPOLOGY:	linear

TYPE OF MOLECULE:	cDNA
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HYPOTHETICAL:	no
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ANTI-SENSE:	no
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ORIGINAL ORIGIN:	
ORGANISM:	Homo sapiens
LINE:	caucasian
DEVELOPMENT STATE:	adult
CELL TYPE:	epidermal keratinocyte

DIRECT ORIGIN:	cDNA from keratinocytes
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CHARACTERISTIC:

NAME/KEY:	coded sequence for regulatory protein from
human keratinocytes	
LOCATION:	from 1 to 2533
DETERMINATION	
METHOD:	cDNA-sequencing

## ANGABEN ZU SEQ ID NO 1 :

## SEQUENZCHARAKTERISTIKA:

LÄNGE:	2533 Basenpaare
ART:	Desoxyribonukleinsäure
TOPOLOGIE:	linear

ART DES MOLEKÜLS:	cDNA
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HYPOTHETISCH:	nein
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ANTI-SENSE:	nein
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## URSPRÜNGLICHE HERKUNFT:

ORGANISMUS:	Homo sapiens
STAMM:	kaukasisch
ENTWICKLUNGSSTADIUM:	adult
ZELLTYP:	epidermaler Keratinozyt

UNMITTELBARE HERKUNFT:	cDNA aus Keratinozyten
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## MERKMAL:

NAME/SCHLÜSSEL:	kodierende Sequenz für regulatorisches Protein aus humanen Keratinozyten
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LAGE:	von 1 bis 2533
ERMITTLUNGSMETHODE:	cDNA-Sequenzierung

## SEQUENCE DESCRIPTION : SEQ ID NO 1 :

```
1   GGCACCCAGG TGC GCGCGGA GCCATGGTTA TCATGTCGGA GTTCAGCGCG
51  GACCCCGCGG GCCAGAGTCA GGGCCAGCAG AAGCCCCTCC GGGTGGGTTT
101 TTACGACATC GAGCGGACCC TGGGCAAAGG CAACTTCGCG GTGGTGAAGC
151 TGGCGCGGCA TCGAGTCACC AAAACGCAGG TTGCAATAAA AATAATTGAT
201 AAAACACGAT TAGATTCAAG CAATTTGGAG AAAATCTATC GTGAGGTTCA
251 GCTGATGAAG CTTCTGAACC ATCCACACAT CATAAAGCTT TACCAGGTTA
301 TGGAAACAAA GGACATGCTT TACATCGTCA CTGAATTTGC TAAAAATGGA
351 GAAATGTTTG ATTATTTGAC TTCCAACGGG CACCTGAGTG AGAACGAGGC
401 GCGGAAGAAG TTCTGGCAAA TCCTGTCGGC CGTGGAGTAC TGTACGACC
451 ATCACATCGT CCACCGGGAC CTCAAGACCG AGAACCTCCT GCTGGATGGC
501 AACATGGACA TCAAGCTGGC AGATTTTGGA TTTGGGAATT TCTACAAGTC
551 AGGAGAGCCT CTGTCCACGT GGTGTGGGAG CCCCCCGTAT GCCGCCCGG
601 AAGTCTTTGA GGGGAAGGAG TATGAAGGCC CCCAGCTGGA CATCTGGAGC
651 CTGGGCGTGG TGCTGTACGT CCTGGTCTGC GGTTCTCTCC CCTTCGATGG
701 GCCTAACCTG CCGACGCTGA GACAGCGGGT GCTGGAGGGC CGCTCCGCA
751 TCCCCTTCTT CATGTCTCAA GACTGTGAGA GCCTGATCCG CCGCATGCTG
801 GTGGTGGACC CCGCCAGGCG CATCACCATC GCCCAGATCC GGCAGCACC
851 GTGGATGCGG GCTGAGCCCT GCTTGCCGGG ACCCGCCTGC CCCGCCTTCT
901 CCGCACACAG CTACACCTCC AACCTGGGCG ACTACGATGA GCAGGCGCTG
951 GGTATCATGC AGACCCTGGG CGTGGACCGG CAGAGGACGG TGGAGTCACT
1001 GCAAAACAGC AGCTATAACC ACTTTGCTGC CATTTATTAC CTCCTCCTTG
1051 AGCGGCTCAA GGAGTATCGG AATGCCCAGT GCGCCCGCCC CGGGCCTGCC
1101 AGGCAGCCGC GGCCTCGGAG CTCGGACCTC AGTGGTTTGG AGGTGCCTCA
1151 GGAAGGTCTT TCCACCGACC CTTTCCGACC TGCCTTGCTG TGCCCGCAGC
1201 CGCAGACCTT GGTGCAGTCC GTCCTCCAGG CCGAGATGGA CTGTGAGCTC
1251 CAGAGCTCGC TGCAGTGGCC CTTGTTCTTC CCGGTGGATG CCAGCTGCAG
1301 CGGAGTGTC CGGCCCCGGC CCGTGTCCCC AAGCAGCCTG CTGGACACAG
1351 CCATCAGTGA GGAGGCCAGG CAGGGGCCGG GCCTAGAGGA GGAGCAGGAC
1401 ACGCAGGAGT CCCTGCCCAG CAGCACGGGC CGGAGGCACA CCCTGGCCGA
1451 GGTCTCCACC CGCCTCTCCC CACTACCGC GCCATGTATA GTCGTCTCCC
1501 CCTCCACCAC GGCAAGTCTT GCAGAGGGAA CCAGCTCTGA CAGTTGTCTG
1551 ACCTTCTCTG CGAGCAAAAG CCCC GCGGGG CTAGTGGCA CCCC GGCAC
1601 TCAGGGGCTG CTGGGCGCCT GTCCTCCGGT CAGGCTGGCC TCGCCCTTCC
1651 TGGGGTCGCA GTCCGCCACC CCAGTGCTGC AGGCTCAGGG GGGCTTGGGA
1701 GGAGCTGTTT TGCTCCCTGT CAGCTTCCAG GAGGGACGGC GGGCGTCGGA
1751 CACCTCACTG ACTCAAGGGC TGAAGGCCTT TCGGCAGCAG CTGAGGAAGA
1801 CCACGCGGAC CAAAGGGTTT CTGGGACTGA ACAAATCAA GGGGCTGGCT
1851 CGCCAGGTGT GCCAGGTCCC TGCCAGCCGG GCCAGCAGGG GCGGCCTGAG
1901 CCCCTTCCAC GCCCCTGCAC AGAGCCCAGG CCTGCACGGC GCGCAGCCG
1951 GCAGCCGGGA GGGCTGGAGC CTGCTGGAGG AGGTGCTAGA GCAGCAGAGG
2001 CTGCTCCAGT TACAGCACCA CCGGCCCGCT GCACCCGGCT GCTCCAGGC
2051 CCCCAGCCG GCCCTGCCG CGTTTGATGAT CGCCCCCTGT GATGGCCCTG
2101 GGGCTGCCCC GCTCCCCAGC ACCCTCCTCA CGTCGGGGCT CCCGCTGCTG
2151 CCGCCCCCAC TCCTGCAGAC CGGCGCGTCC CCGGTGGCCT CAGCGGCGCA
2201 GCTCCTGGAC ACACACCTGC ACATTGGCAC CGGCCCCACC GCCCTCCCCG
2251 CTGTGCCCCC ACCACGCCTG GCCAGGCTGG CCCCAGGTTG TGAGCCCCTG
2301 GGGCTGCTGC AGGGGGACTG TGAGATGGAG GACCTGATGC CCTGCTCCCT
2351 AGGCACGTTT GTCCTGGTGC AGTGAGGGCA GCCCTGCATC CTGGCACGGA
2401 CACTGACTCT TACAGCAATA ACTTCAGAGG AGGTGAAGAC ATCTGGCCTC
2451 AAAGCCAAGA ACTTTCTAGA AGCGAAATAA GCAATACGTT AGGTGTTTGG
2501 GCGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA
```

## DETAILS FOR SEQ ID NO 2

## SEQUENCE CHARACTERISTICS

LENGTH: 790 Amino Acids  
TYPE: amino acid sequence

TYPE OF MOLECULE: protein

## ORIGINAL ORIGIN:

ORGANISM: Homo sapiens  
LINE: caucasian  
DEVELOPMENT STATE: adult  
CELL TYPE: epidermal keratinocyte

DIRECT ORIGIN: derived from cDNA sequence

## CHARACTERISTIC:

NAME/KEY: coded sequence for regulatory protein from  
human keratinocytes  
LOCATION: from 1 to 790  
DETERMINATION  
METHOD: Derivation from cDNA-sequencing  
OTHER DETAILS: includes a Serine/Threonine-Kinase Motif,  
Four Tyrosine kinase phosphorylation motifs and  
a kinase domain with ATP binding site

## SEQUENCE DESCRIPTION : SEQ ID NO 2 :

1 HPGARGAMVI MSEFSADPAG QSQGQOKPLR VGFYDIERTL GKGNFAVVKL  
51 ARHRVTKTQV AIKIIDKTRL DSSNLEKIYR EVQLMKLLNH PHIICKLYQVM  
101 ETKDMLYIVT EFAKNGEMFD YLTSNGHLSE NEARKKFWQI LSAVEYCHDH  
151 HIVHRDLKTE NLLLDGNMDI KLADFGFGNF YKSGEPLSTW CGSPPYAAPE  
201 VFEGKEYEGP QLDIWSLGVV LYVLVCGSLP FDGPNLPTLR QRVLEGRFRI  
251 PFFMSQDCES LIRRMLVUDP ARRITIAQIR QHRWMRAEPC LPGPACPAFS  
301 AHSYTSNLGD YDEQALGIMQ TLGVDRQRTV ESLQNSSYNH FAAIYYLLLE  
351 RLKEYRNAQC ARPGPARQPR PRSSDLSGLE VPQEGLSTDP FRPALLCPQP  
401 QTLVQSVLQA EMDCELQSSL QWPLFFPVDA SCSGVFRPRP VSPSSLLDTA  
451 ISEEARQGP G LEEEQDTQES LPSSTGRRHT LAEVSTRLSP LTAPCIVVSP  
501 STTASPAEGT SSDSCLTFSA SKSPAGLSGT PATQGLLGAC SPVRLASPFL  
551 GSQSATPVLQ AQGGLGGAVL LPVSFQEGRR ASDTSLTQGL KAFRQQLRKT  
601 TRTKGFLGLN KIKGLARQVC QVPASRASRG GLSPFHAPAQ SPGLHGGAAG  
651 SREGWSLLEE VLEQQRLLQL QHHPAAAPGC SQAPQPAPAP FVIAPCDGPG  
701 AAPLPSTLLT SGLPLLPPPL LQTGASPVAS AAQLLDTHLH IGTGPTALPA  
751 VPPPRLARLA PGCEPLGLLQ GDCEMEDLMP CSLGTFVLVQ

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DETAILS FOR SEQ ID NO 3:

SEQUENCE CHARACTERISTICS

LENGTH:

7823 Amino Acids

TYPE:

amino acid sequence

TYPE OF MOLECULE:

protein

ORIGINAL ORIGIN:

ORGANISM:

Homo sapiens

LINE:

caucasian

DEVELOPMENT STATE:

adult

CELL TYPE:

epidermal keratinocyte

DIRECT ORIGIN:

derived from cDNA sequence

CHARACTERISTIC:

NAME/KEY:

coded sequence for regulatory protein from

human keratinocytes

LOCATION:

from 1 to 823

DETERMINATION

METHOD:

Derivation from cDNA-sequencing

OTHER DETAILS:

includes a Serine/Threonine-Kinase Motif,  
Four Tyrosine kinase phosphorylation motifs and  
a kinase domain with ATP binding site

## SEQUENCE DESCRIPTION : SEQ ID NO 3 :

1 PEAIAAIAAIA GAVGTRAAPA AERAASWPGR SGGGGGARGA MVIMSEFSAD  
51 PAGQSOGQOK SLRVGFYDIE RTLKGKNFAV VKLARHRVTK TQVAIKIIDK  
101 TRLDSSNLEK IYREVQLMKL LNHPIIIKLY QVMETKDMLY IVTEFAKNGE  
151 MFDYLTSNGH LSENEARKKF WQILSAVEYC HDHHIVHRDL KTENLLLDGN  
201 MDIKLADFGF GNFYKSGEPL STWCGSPPYA APEVFEGKEY EGPQLDIWSL  
251 GVVLYVLVCG SLPFDGPNLP TLRQRVLEGR FRIPFFMSQD CESLIRRMIV  
301 VDPARRITIA QIRQHRWMRA EPCLPGPACP AFSAHSYTSN LGDYDEQALG  
351 IMQTLGVDRQ RTVESLQNSS YNHFAAIYYL LLERLKEYRN AQCARPGPAR  
401 QPRPRSSDLS GLEVPQEGLS TDPFRPALLC PQPQTLVQSV LQAEMDCELQ  
451 SSLQWPLFFP VDASC SGVFR PRPVSPSSLL DTAISEEARQ GPGLEEEQDT  
501 QESLPSSTGR RHTLAEVSTR LSPLTAPCIV VSPSTTASPA EGTSSDSCLT  
551 FSASKSPAGL SGTPATQGLL GACSPVRLAS PFLGSQSATP VLQAQGGLGG  
601 AVLLPVSFQE GRRASDTSLT QGLKAFRQQL RKTTRTKGFL GLNKIKGLAR  
651 QVCQVPASRA SRGGLSPFHA PAQSPGLHGG AAGSREGWSL LEEVLEQQRL  
701 LQLQHHPAAA PGCSQAPQPA PAFVFIAPCD GPGAAPLPST LLTSGLPLLP  
751 PPLLQTGASP VASAAQLLDT HLHIGTGPTA LPAVPPPRLA RLAPGCEPLG  
801 LLQGDCEMED LMPCSLGTFV LVQ



## DETAILS FOR SEQ ID NO 4:

## SEQUENCE CHARACTERISTICS

LENGTH:	2632 Base Pairs
TYPE:	deoxyribonucleic acid
TOPOLOGY:	linear

TYPE OF MOLECULE:	cDNA
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HYPOTHETICAL:	no
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ANTI-SENSE:	no
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## ORIGINAL ORIGIN:

ORGANISM:	Homo sapiens
LINE:	caucasian
DEVELOPMENT STATE:	adult
CELL TYPE:	epidermal keratinocyte

DIRECT ORIGIN:	cDNA from keratinocytes
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## CHARACTERISTIC:

NAME/KEY:	coded sequence for regulatory protein from
human keratinocytes	
LOCATION:	from 1 to 2632
DETERMINATION METHOD:	cDNA-sequencing

## SEQUENCE DESCRIPTION : SEQ ID NO 4 :

```
1  CCCCCGAGGC AGCAGCAGCG GCGGCGGCAG CCGGAGCAGT AGGCACCCGA
51  GCAGCGCCAG CGGCCGAGCG GCGCGCTTCC TGGCCTGGGC GCTCCGGTGG
101 CGGCGGAGGT GCGCGCGGAG CCATGGTTAT CATGTCGGAG TTCAGCGCGG
151 ACCCCGCGGG CCAGAGTCAG GGCCAGCAGA AGTCCCTCCG GGTGGGTTTT
201 TACGACATCG AGCGGACCCT GGGCAAAGGC AACTTCGCGG TGGTGAAGCT
251 GCGCGGGCAT CGAGTCACCA AAACGCAGGT TGCAATAAAA ATAATTGATA
301 AAACACGATT AGATTCAAGC AATTTGGAGA AAATCTATCG TGAGGTTTCA
351 CTGATGAAGC TTCTGAACCA TCCACACATC ATAAAGCTTT ACCAGGTTAT
401 GGAAACAAAG GACATGCTTT ACATCGTCAC TGAATTTGCT AAAAATGGAG
451 AAATGTTTGA TTATTTGACT TCCAACGGGC ACCTGAGTGA GAACGAGGCG
501 CGGAAGAAAT TCTGGCAAAT CCTGTCGGCC GTGGAGTACT GTCACGACCA
551 TCACATCGTC CACCGGGACC TCAAGACCGA GAACCTCCTG CTGGATGGCA
601 ACATGGACAT CAAGCTGGCA GATTTTGGAT TTGGGAATTT CTACAAGTCA
651 GGAGAGCCTC TGTCCACGTG GTGTGGGAGC CCCCCGTATG CCGCCCCGGA
701 AGTCTTTGAG GGAAGGAGT ATGAAGGCC CCAGCTGGAC ATCTGGAGCC
751 TGGGCGTGGT GCTGTACGTC CTGGTCTGCG GTTCTCTCCC CTTCGATGGG
801 CCTAACCTGC CGACGCTGAG ACAGCGGGTG CTGGAGGGCC GCTTCCGCAT
851 CCCCTTCTTC ATGTCTCAAG ACTGTGAGAG CCTGATCCGC CGCATGCTGG
901 TGGTGGACCC CGCCAGGCGC ATCACCATCG CCCAGATCCG GCAGACCCGG
951 TGGATGCGGG CTGAGCCCTG CTTGCCGGGA CCCGCCTGCC CCGCCTTCTC
1001 CGCACACAGC TACACCTCCA ACCTGGGCGA CTACGATGAG CAGGCGCTGG
1051 GTATCATGCA GACCCTGGGC GTGGACCGGC AGAGGACGGT GGAGTCACTG
1101 CAAAACAGCA GCTATAACCA CTTTGCTGCC ATTTATTACC TCCTCCTTGA
1151 GCGGCTCAAG GAGTATCGGA ATGCCAGTG CGCCCGCCCC GGGCCTGCCA
1201 GGCAGCCGCG GCCTCGGAGC TCGGACCTCA GTGGTTTGA GGTGCCTCAG
1251 GAAGGTCTTT CCACCGACCC TTTCCGACCT GCCTTGCTGT GCCCGCAGCC
1301 GCAGACCTTG GTGCAGTCCG TCCTCCAGGC CGAGATGGAC TGTGAGCTCC
1351 AGAGCTCGCT GCAGTGGCCC TTGTTCTTCC CGGTGGATGC CAGCTGCAGC
1401 GGAGTGTTCC GGCCCCGGCC CGTGTCCCA AGCAGCCTGC TGGACACAGC
1451 CATCAGTGAG GAGGCCAGGC AGGGGCCGGG CCTAGAGGAG GAGCAGGACA
1501 CGCAGGAGTC CCTGCCCAGC AGCACGGGCC GGAGGCACAC CCTGGCCGAG
1551 GTCTCCACCC GCCTCTCCCC ACTCACCGCG CCATGTATAG TCGTCTCCCC
1601 CTCCACCACG GCAAGTCCTG CAGAGGGAAC CAGCTCTGAC AGTTGTCTGA
1651 CCTTCTCTGC GAGCAAAGC CCCGCGGGG TCAGTGGCAC CCCGGCCACT
1701 CAGGGGCTGC TGGGCGCCTG CTCCCCGGTC AGGCTGGCCT CGCCCTTCTC
1751 GGGGTGCGAG TCCGCCACCC CAGTGCTGCA GGCTCAGGGG GGCTTGGGAG
1801 GAGCTGTTCT GCTCCCTGTC AGCTTCCAGG AGGGACGGCG GCGTCGGAC
1851 ACCTCACTGA CTAAGGGCT GAAGGCCTTT CGGCAGCAGC TGAGGAAGAC
1901 CACGCGGACC AAAGGGTTTC TGGGACTGAA CAAAATCAAG GGGCTGGCTC
1951 GCCAGGTGTG CCAGGTCCCT GCCAGCCGGG CCAGCAGGGG CGGCCTGAGC
2001 CCCTTCCACG CCCCTGCACA GAGCCCAGGC CTGCACGGCG GCGCAGCCGG
2051 CAGCCGGGAG GGCTGGAGCC TGCTGGAGGA GGTGCTAGAG CAGCAGAGGC
2101 TGCTCCAGTT ACAGCACCAC CCGGCCGCTG CACCCGGCTG CTCCCAGGCC
2151 CCCCAGCCGG CCCCTGCCCC GTTTGTGATC GCCCCCTGTG ATGGCCCTGG
2201 GGCTGCCCCG CTCCCAGCA CCCTCCTCAC GTCGGGGCTC CCGCTGCTGC
2251 CGCCCCCACT CCTGCAGACC GGCGCGTCCC CGGTGGCCTC AGCGGCGCAG
2301 CTCCTGGACA CACACCTGCA CATTGGCACC GGCCCCACCG CCCTCCCCGC
2351 TGTGCCCCCA CCACGCCTGG CCAGGCTGGC CCCAGGTTGT GAGCCCTGG
2401 GGCTGCTGCA GGGGGACTGT GAGATGGAGG ACCTGATGCC CTGCTCCCTA
2451 GGCACGTTTG TCCTGGTGCA GTGAGGGCAG CCCTGCATCC TGGCACGGAC
2501 ACTGACTCTT ACAGCAATAA CTTAGAGGA GGTGAAGACA TCTGGCCTCA
2551 AAGCCAAGAA CTTTCTAGAA GCGAAATAAG CAATACGTTA GGTGTTTTGG
2601 CGAAAAA AAAA AAAAAA AA
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